

**REMARKS**

Entry of the foregoing amendment, reconsideration and reexamination of the subject application, as amended, pursuant to and consistent with 37 CFR §1.112, and in light of the remarks which follows, are respectfully requested.

By the present amendments, the present title has been cancelled in favor of a new, non-descriptive title. Additionally, claim 1 has been amended in order to obviate the §101 utility and §112, second paragraph rejections.

**IN THE TITLE**

Cancel the current title and substitute therefore:

--Methods for Mapping the Genomic of An Avion Using Isolated  
Z-Chromosomal DNA's--

Turning now to the Office Action, the objection to the title is noted. It is anticipated that this rejection shall be moot in view of the present amendment.

Claim 1 stands rejected under 35 U.S.C. §101 as not being based on a specific and substantial utility. It is also anticipated that this rejection shall be moot upon entry of this amendment.

In the subject final rejection, the Examiner has rejected claim 1 which was previously directed to DNA sequences pre se as not being based on a credible utility. The Examiner acknowledges that Z-Chromosomal sequences can be used to identify particular chromosomal arrangements in the turkey genome but indicates that this is not a sufficient or substantive enough utility to support the utility requirement

under §101 for the DNAs per se. (The Examiner acknowledges, however, that this application of the claimed Z-chromosomal DNA would be applicable to Z-chromosomal sequences in general.)

However, Applicant respectfully note that the current claim is now directed to a method of mapping the genome of a turkey using specific Z-chromosomal DNA sequences which are identified and sequenced herein. As acknowledged by the Examiner, it would be anticipated based on the teachings of this application, that these sequences can be used in the manner claimed. Specifically, as evidenced by the microsatellite marker depicted in Figure 2 these sequences together form a library which can be used to identify the chromosomal rearrangement in sex-linkage genotypes. This application of the subject DNAs is supported by Reguigne-Arnold et al. (Genomics, 1996, 32(3): 458-61; and Ye et al., Genomics 28(3): 566-569 (1995). Accordingly, based on the Examiner's acquiescence on this issue, and the present amendment, as further supported by the cited references, withdrawal of the §101 rejection is believed to be in order.

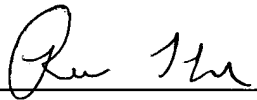
Claim 1 further stands rejected under 35 U.S.C. §112 second paragraph as being indefinite. This rejection is based on the same reasoning as the §101 rejection. Accordingly, it is anticipated that this rejection is obviated by the present amendment.

Based on the foregoing, this application is believed to be in condition for allowance. A Notice to this effect is respectfully solicited. However, if any issues

remain outstanding after consideration of this reply, the Examiner is respectfully requested to contact the undersigned.

Respectfully submitted,

July 14, 2003

  
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